



OIRP

RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/09/934,323

TIME: 18:31:14

Input Set : A:\10448-081001.TXT

Output Set: N:\CRF3\02072002\I934323.raw

P.S

4 <110> APPLICANT: Curtis, Rory A. J.
 6 <120> TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
 7 FAMILY MEMBER AND USES THEREOF
 10 <130> FILE REFERENCE: 10448-081001
 12 <140> CURRENT APPLICATION NUMBER: US 09/934,323
 13 <141> CURRENT FILING DATE: 2001-08-21
 15 <150> PRIOR APPLICATION NUMBER: US 60/226,774
 16 <151> PRIOR FILING DATE: 2000-08-21
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4667
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (420)...(2924)
 31 <400> SEQUENCE: 1

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34	tctgtccgtc tgtctgtatc ctgcctccct gccctctctg ctccaccccc cgcaggtcgg	180
35	gcctgccttc accttctccc atttcccttc ccttccccac ccctgtcccc ctccatggag	240
36	aggaacagac cccttctctg tccagtctaa cccagggtccc tccccaaccc cctcctccct	300
37	cctttccccc cgcctctctt cctcctctgg gcgagggggg cctcctcccc tctccccccc	360
38	ttctctctct ctccgagggg ggggggtccc agggagggag ggggggtccc ccgatcagc	419
39	atg tgg ctc ctg gcg ctg tgt ctg ggg ctg gcg ggg gct caa cgc	467
40	Met Trp Leu Leu Ala Leu Cys Leu Val Gly Leu Ala Gly Ala Gln Arg	
41	1 5 10 15	
43	ggg gga ggg ggt ccc ggc ggc ggc gcc ccg ggc ggc ccc ggc ctg ggc	515
44	Gly Gly Gly Gly Pro Gly Gly Gly Ala Pro Gly Gly Pro Gly Leu Gly	
45	20 25 30	
47	ctc ggc agc ctc ggc gag gag cgc ttc ccg gtg gtg aac acg gcc tac	563
48	Leu Gly Ser Leu Gly Glu Glu Arg Phe Pro Val Val Asn Thr Ala Tyr	
49	35 40 45	
51	ggg cga gtg cgc ggt gtg cgg cgc gag ctc aac aac gag atc ctg ggc	611
52	Gly Arg Val Arg Gly Val Arg Arg Glu Leu Asn Asn Glu Ile Leu Gly	
53	50 55 60	
55	ccc gtc gtg cag ttc ttg ggc gtg ccc tac gcc acg ccg ccc ctg ggc	659
56	Pro Val Val Gln Phe Leu Gly Val Pro Tyr Ala Thr Pro Pro Leu Gly	
57	65 70 75 80	
59	gcc cgc cgc ttc cag ccg cct gag gcg ccc gcc tcg tgg ccc ggc gtg	707
60	Ala Arg Arg Phe Gln Pro Pro Glu Ala Pro Ala Ser Trp Pro Gly Val	
61	85 90 95	

ENTERED

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63	cg	ac	gc	acc	acc	ctg	ccg	ccc	gcc	tgc	ccg	cag	aac	ctg	cac	ggg	755
64	Arg	Asn	Ala	Thr	Thr	Leu	Pro	Pro	Ala	Cys	Pro	Gln	Asn	Leu	His	Gly	
65				100					105					110			
67	gcg	ctg	ccc	gcc	atc	atg	ctg	cct	gtg	tgg	ttc	acc	gac	aac	ttg	gag	803
68	Ala	Leu	Pro	Ala	Ile	Met	Leu	Pro	Val	Trp	Phe	Thr	Asp	Asn	Leu	Glu	
69			115				120						125				
71	gcg	gcc	gcc	acc	tac	gtg	cag	aac	cag	agc	gag	gac	tgc	ctg	tac	ctc	851
72	Ala	Ala	Ala	Thr	Tyr	Val	Gln	Asn	Gln	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	
73			130				135						140				
75	aac	ctc	tac	gtg	ccc	acc	gag	gac	ggg	ccg	ctc	aca	aaa	aaa	cgt	gac	899
76	Asn	Leu	Tyr	Val	Pro	Thr	Glu	Asp	Gly	Pro	Leu	Thr	Lys	Lys	Arg	Asp	
77	145					150					155					160	
79	gag	gcg	acg	ctc	aat	ccg	cca	gac	aca	gat	atc	cgt	gac	cct	ggg	aag	947
80	Glu	Ala	Thr	Leu	Asn	Pro	Pro	Asp	Thr	Asp	Ile	Arg	Asp	Pro	Gly	Lys	
81				165						170					175		
83	aag	cct	gtg	atg	ctg	ttt	ctc	cat	ggc	ggc	tcc	tac	atg	gag	ggg	acc	995
84	Lys	Pro	Val	Met	Leu	Phe	Leu	His	Gly	Gly	Ser	Tyr	Met	Glu	Gly	Thr	
85			180						185					190			
87	gga	aac	atg	ttc	gat	ggc	tca	gtc	ctg	gct	gcc	tat	ggc	aac	gtc	att	1043
88	Gly	Asn	Met	Phe	Asp	Gly	Ser	Val	Leu	Ala	Ala	Tyr	Gly	Asn	Val	Ile	
89			195				200						205				
91	gta	gcc	acg	ctc	aac	tac	cgt	ctt	ggg	gtg	ctc	ggg	ttt	ctc	agc	acc	1091
92	Val	Ala	Thr	Leu	Asn	Tyr	Arg	Leu	Gly	Val	Leu	Gly	Phe	Leu	Ser	Thr	
93			210				215						220				
95	ggg	gac	cag	gct	gca	aaa	ggc	aac	tat	ggg	ctc	ctg	gac	cag	atc	cag	1139
96	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Gln	Ile	Gln	
97	225				230					235				240			
99	gcc	ctg	cg	tgg	ctc	agt	gaa	aac	atc	gcc	cac	ttt	ggg	ggc	gac	ccc	1187
100	Ala	Leu	Arg	Trp	Leu	Ser	Glu	Asn	Ile	Ala	His	Phe	Gly	Gly	Asp	Pro	
101				245						250				255			
103	gag	cgt	atc	acc	atc	ttt	ggg	tcc	ggg	gca	ggg	gcc	tcc	tgc	gtc	aac	1235
104	Glu	Arg	Ile	Thr	Ile	Phe	Gly	Ser	Gly	Ala	Gly	Ala	Ser	Cys	Val	Asn	
105			260						265					270			
107	ctt	ctg	atc	ctc	tcc	cac	cat	tca	gaa	ggg	ctg	ttc	cag	aag	gcc	atc	1283
108	Leu	Leu	Ile	Leu	Ser	His	His	Ser	Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	
109			275					280					285				
111	gcc	cag	agt	ggc	acc	gcc	att	tcc	agc	tgg	tct	gtc	aac	tac	cag	ccg	1331
112	Ala	Gln	Ser	Gly	Thr	Ala	Ile	Ser	Ser	Trp	Ser	Val	Asn	Tyr	Gln	Pro	
113			290				295					300					
115	ctc	aag	tac	acg	cgg	ctg	ctg	gca	gcc	aag	gtg	ggc	tgt	gac	cga	gag	1379
116	Leu	Lys	Tyr	Thr	Arg	Leu	Leu	Ala	Ala	Lys	Val	Gly	Cys	Asp	Arg	Glu	
117	305					310					315				320		
119	gac	agt	gct	gaa	gct	gtg	gag	tgt	ctg	cg	cgg	aag	ccc	tcc	cgg	gag	1427
120	Asp	Ser	Ala	Glu	Ala	Val	Glu	Cys	Leu	Arg	Arg	Lys	Pro	Ser	Arg	Glu	
121			325						330					335			
123	ctg	gtg	gac	cag	gac	gtg	cag	cct	gcc	cg	tac	cac	atc	gcc	ttt	ggg	1475
124	Leu	Val	Asp	Gln	Asp	Val	Gln	Pro	Ala	Arg	Tyr	His	Ile	Ala	Phe	Gly	
125			340						345					350			
127	ccc	gtg	gtg	gat	ggc	gac	gtg	gtc	ccc	gat	gac	cct	gag	atc	ctc	atg	1523

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128	Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile	Leu	Met	
129			355					360					365				
131	cag	cag	gga	gaa	ttc	ctc	aac	tac	gac	atg	ctc	atc	ggc	gtc	aac	cag	1571
132	Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val	Asn	Gln	
133		370					375					380					
135	gga	gag	ggc	ctc	aag	ttc	gtg	gag	gac	tct	gca	gag	agc	gag	gac	ggt	1619
136	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu	Asp	Gly	
137	385					390					395					400	
139	gtg	tct	gcc	agc	gcc	ttt	gac	ttc	act	gtc	tcc	aac	ttt	gtg	gac	aac	1667
140	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val	Asp	Asn	
141					405					410					415		
143	ctg	tat	ggc	tac	ccg	gaa	ggc	aag	gat	gtg	ctt	cgg	gag	acc	atc	aag	1715
144	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr	Ile	Lys	
145			420						425					430			
147	ttt	atg	tac	aca	gac	tgg	gcc	gac	cgg	gac	aat	ggc	gaa	atg	cgc	cgc	1763
148	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met	Arg	Arg	
149			435					440					445				
151	aaa	acc	ctg	ctg	gcg	ctc	ttt	act	gac	cac	caa	tgg	gtg	gca	cca	gct	1811
152	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala	Pro	Ala	
153		450					455					460					
155	gtg	gcc	act	gcc	aag	ctg	cac	gcc	gac	tac	cag	tct	ccc	gtc	tac	ttt	1859
156	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val	Tyr	Phe	
157	465					470					475					480	
159	tac	acc	ttc	tac	cac	cac	tgc	cag	gcg	gag	ggc	cgg	cct	gag	tgg	gca	1907
160	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu	Trp	Ala	
161					485					490					495		
163	gat	gcg	gcg	cac	ggg	gat	gaa	ctg	ccc	tat	gtc	ttt	ggc	gtg	ccc	atg	1955
164	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val	Pro	Met	
165			500						505					510			
167	gtg	ggt	gcc	acc	gac	ctc	ttc	ccc	tgt	aac	ttc	tcc	aag	aat	gac	gtc	2003
168	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn	Asp	Val	
169		515						520					525				
171	atg	ctc	agt	gcc	gtg	gtc	atg	acc	tac	tgg	acc	aac	ttc	gcc	aag	act	2051
172	Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala	Lys	Thr	
173		530					535					540					
175	ggg	gac	ccc	aac	cag	ccg	gtg	ccg	cag	gat	acc	aag	ttc	atc	cac	acc	2099
176	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile	His	Thr	
177	545				550					555						560	
179	aag	ccc	aat	cgc	ttc	gag	gag	gtg	gtg	tgg	agc	aaa	ttc	aac	agc	aag	2147
180	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn	Ser	Lys	
181				565					570					575			
183	gag	aag	cag	tat	ctg	cac	ata	ggc	ctg	aag	cca	cgc	gtg	cgt	gac	aac	2195
184	Glu	Lys	Gln	Tyr	Leu	His	Ile	Gly	Leu	Lys	Pro	Arg	Val	Arg	Asp	Asn	
185			580						585					590			
187	tac	cgc	gcc	aac	aag	gtg	gcc	ttc	tgg	ctg	gag	ctc	gtg	ccc	cac	ctg	2243
188	Tyr	Arg	Ala	Asn	Lys	Val	Ala	Phe	Trp	Leu	Glu	Leu	Val	Pro	His	Leu	
189		595					600					605					
191	cac	aac	ctg	cac	acg	gag	ctc	ttc	acc	acc	acc	acg	cgc	ctg	cct	ccc	2291
192	His	Asn	Leu	His	Thr	Glu	Leu	Phe	Thr	Thr	Thr	Thr	Arg	Leu	Pro	Pro	

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195 tac gcc acg cgc tgg ccg cct cgt ccc ccc gct ggc gcc ccg ggc aca      2339
196 Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro Gly Thr
197 625      630      635      640
199 cgc cgg ccc ccg ccg cct gcc acc ctg cct ccc gag ccc gag ccc gag      2387
200 Arg Arg Pro Pro Pro Pro Ala Thr Leu Pro Pro Glu Pro Glu Pro Glu
201      645      650      655
203 ccc ggc cca agg gcc tat gac cgc ttc ccc ggg gac tca cgg gac tac      2435
204 Pro Gly Pro Arg Ala Tyr Asp Arg Phe Pro Gly Asp Ser Arg Asp Tyr
205      660      665      670
207 tcc acg gag ctg agc gtc acc gtg gcc gtg ggt gcc tcc ctc ctc ttc      2483
208 Ser Thr Glu Leu Ser Val Thr Val Ala Val Gly Ala Ser Leu Leu Phe
209      675      680      685
211 ctc aac atc ctg gcc ttt gct gcc ctc tac tac aag cgg gac cgg cgg      2531
212 Leu Asn Ile Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Arg Asp Arg Arg
213      690      695      700
215 cag gag ctg cgg tgc agg cgg ctt agc cca cct ggc ggc tca ggc tct      2579
216 Gln Glu Leu Arg Cys Arg Arg Leu Ser Pro Pro Gly Gly Ser Gly Ser
217 705      710      715      720
219 ggc gtg cct ggt ggg ggc ccc ctg ctc ccc gcc gcg ggc cgt gag ctg      2627
220 Gly Val Pro Gly Gly Gly Pro Leu Leu Pro Ala Ala Gly Arg Glu Leu
221      725      730      735
223 cca cca gag gag gag ctg gtg tca ctg cag ctg aag cgg ggt ggt ggc      2675
224 Pro Pro Glu Glu Glu Leu Val Ser Leu Gln Leu Lys Arg Gly Gly Gly
225      740      745      750
227 gtc ggg gcg gac cct gcc gag gct ctg cgc cct gcc tgc ccg ccc gac      2723
228 Val Gly Ala Asp Pro Ala Glu Ala Leu Arg Pro Ala Cys Pro Pro Asp
229      755      760      765
231 tac acc ctg gcc ctg cgc cgg gca ccg gac gat gtg cct ctc ttg gcc      2771
232 Tyr Thr Leu Ala Leu Arg Arg Ala Pro Asp Asp Val Pro Leu Leu Ala
233      770      775      780
235 ccc ggg gcc ctg acc ctg ctg ccc agt ggc ctg ggg cca ccg cca ccc      2819
236 Pro Gly Ala Leu Thr Leu Leu Pro Ser Gly Leu Gly Pro Pro Pro Pro
237 785      790      795      800
239 cca ccg ccc ccc tcc ctt cat ccc ttc ggg ccc ttc ccc ccg ccc cct      2867
240 Pro Pro Pro Pro Ser Leu His Pro Phe Gly Pro Phe Pro Pro Pro Pro
241      805      810      815
243 ccc acc gcc acc agc cac aac aac acg cta ccc cac ccc cac tcc acc      2915
244 Pro Thr Ala Thr Ser His Asn Asn Thr Leu Pro His Pro His Ser Thr
245      820      825      830
247 act cgg gta taggggggtgg gtggggaggc cctcctcccc ggccctccct      2964
248 Thr Arg Val
249      835
251 ggcccgcca ctccgaaggc agggaggagg acttggaac tggcttttct cctgtggagt      3024
252 cgtcacacgc catccagcag cgctaagggtg gacatgggat tcctccctgc gatgcgtgtc      3084
253 tttccacgc agagaagccc cagtctcttc tctggatctg ggcctttgaa caactggggg      3144
254 gcgttttctc cccccattg ggacaccagt cttcggtgtg tggaatgtg tattttcccg      3204
255 cgtggagggtg tgctttctca caacgggggtg tgttttccca tgtgcagggt gaggtttttt      3264
256 tttgccaccc tggacacatg ttggccccct caaagaattt ctgtggggat ttgtacccca      3324

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257 gaatcctggt ccccatccc ttctcccacc tcctcccctc tccctccccc tggagaccct 3384
258 ggaagtgggt tgttcacata cagtgaacct tggccaccag accacagagg atggagcctg 3444
259 ggaagcagcg aggaaatcac agccccctcg cccctgcctc ccttgccctt accccggcga 3504
260 agcatgttcc ccccgacgcc ccccttgcca caagtcagat gaagcaogtt ctgccgggga 3564
261 ggccctcacc ttccagagag gacagacaca gatttctgc tgggggaggg aggagtccac 3624
262 gcatcctgat gctgcctgga agcttatttt cccgtggcca ggacgcattt ctctgagtgg 3684
263 aaacaggttc ttgcatgtgg atgtgtgttt cccagggcag acggccctc tcttcccagc 3744
264 acttccctgc ctccccagg cctcaggccc agcaccagt tctcctcac atggcagggtg 3804
265 agcacagact tctagtgtgg aggagctgag gaggggtgaac aaaccccgag ggaggcccg 3864
266 cccttgctcc cgagttgggg ggaggggggtg tggcaacgtg ccccccgcag aggccacgca 3924
267 tgtttgacca aagccctcat tgtggtccga ggacagcctt tccccaggc ctacagagcat 3984
268 tgctcatccg tgccaaactg gtaggtgga tttgagcgga aagactccca aaatgtgcca 4044
269 agaatttccc agtcccaggc agggcagggg aaactaaggg caagcaggat acagggcgag 4104
270 ggatgtggca ggtgaggggg ctccgcctg tgcctctct cctcaccatg tctccccac 4164
271 cctgcctcag ttctccgttc ccttcatct ccttccctt cgttgaagct gtccccatct 4224
272 cagtgtcaga ccagccttct cctcatctga ccacctct ctgaccgacg cccctcctt 4284
273 gtctgaaaga aaggagcctt gaatggtgga gggaggcagt ggggagaaag gtctcaccgg 4344
274 acaggttggg agaatgaggt cagcgtgtgt ggggaacaga tggagggggc agtggggaca 4404
275 gggcttgggc agacaccagc aggaataatt tgaaatgtgt gaggtgactc cccggagggc 4464
276 cttgggcttg ggcatttggg aaaagaatga tgtctggaag ggcttaaggg acacagtgga 4524
277 cgaggggaga gtcctcatct gctggcattt tgtggggtgt tagtgccaaa cttgaatagg 4584
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279 actttgcctc ttgactgtcc ctc 4667

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281 <210> SEQ ID NO: 2

282 <211> LENGTH: 835

283 <212> TYPE: PRT

284 <213> ORGANISM: Homo sapiens

286 <400> SEQUENCE: 2

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290 20 25 30
291 Leu Gly Ser Leu Gly Glu Glu Arg Phe Pro Val Val Asn Thr Ala Tyr
292 35 40 45
293 Gly Arg Val Arg Gly Val Arg Arg Glu Leu Asn Asn Glu Ile Leu Gly
294 50 55 60
295 Pro Val Val Gln Phe Leu Gly Val Pro Tyr Ala Thr Pro Pro Leu Gly
296 65 70 75 80
297 Ala Arg Arg Phe Gln Pro Pro Glu Ala Pro Ala Ser Trp Pro Gly Val
298 85 90 95
299 Arg Asn Ala Thr Thr Leu Pro Pro Ala Cys Pro Gln Asn Leu His Gly
300 100 105 110
301 Ala Leu Pro Ala Ile Met Leu Pro Val Trp Phe Thr Asp Asn Leu Glu
302 115 120 125
303 Ala Ala Ala Thr Tyr Val Gln Asn Gln Ser Glu Asp Cys Leu Tyr Leu
304 130 135 140
305 Asn Leu Tyr Val Pro Thr Glu Asp Gly Pro Leu Thr Lys Lys Arg Asp
306 145 150 155 160
307 Glu Ala Thr Leu Asn Pro Pro Asp Thr Asp Ile Arg Asp Pro Gly Lys

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8